RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/089,211A*

Source: *1FWJ16*

Date Processed by STIC: *9/17/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/089,211A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 09/17/2004
PATENT APPLICATION: **US/10/089,211A**   TIME: 10:04:37

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

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 3 <110> APPLICANT: University of Victoria Innovation and Developement Corporation
 4        Hintz, William E.
 5        Eades, Caleb Joshua
 7 <120> TITLE OF INVENTION: Mannosidases and Methods for using the Same
 9 <130> FILE REFERENCE: 2847-62447-01
11 <140> CURRENT APPLICATION NUMBER: 10/089,211A
12 <141> CURRENT FILING DATE: 2002-03-25
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/27210
15 <151> PRIOR FILING DATE: 2000-10-02
17 <150> PRIOR APPLICATION NUMBER: 60/157,341
18 <151> PRIOR FILING DATE: 1999-10-01
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3328
26 <212> TYPE: DNA
27 <213> ORGANISM: Aspergillus nidulans
29 <400> SEQUENCE: 1
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34 ctgggcttgg tatgagattg cgagcatcta tgtcggtgta ccttctgaat gacaatgaat     180
36 gtattttact tctcgaaaag aacccttggg cactgaattg tgcggagaat gatgccctga     240
38 ttatgataca actagtccgc tccgtcaagc cacaagggtc tgggcagtcc gctataaatc     300
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62 tacacagatt cagatgacag cccaactccg tcaaaagaac gcctggacac cccgagcaat    1020
64 gtcccatctc aggagcctga atttgatgcc gccagacttc agacgggtgc gcagacccaa    1080
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68 cggcatccag tcagtccgga ggctttgatc aagctgccaa ccgggcaatc aaaggaactc    1200
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72 caacttgaca ctatcaagtc ggcgttctta catgcgtgga acggttacaa gatctctgcc    1320
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76 ggcgcgaccc ttgtcgacgc cttggatacc ctgtggatca tggatctcaa agaggagttc    1440
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RAW SEQUENCE LISTING　　　　　　DATE: 09/17/2004
PATENT APPLICATION:　**US/10/089,211A**　　TIME: 10:04:37

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

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 86 tcagagtttc gccggggcga ctttaaggct gttctcgccg agcttggctc tctctctctc   1740
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122 gcgctctcgc acgaggaatt cgtcacggga aaaatcctca acgaccgact cccgccgggc   2820
124 atgacaggga tctcggctcg gcagtacctc cttcgcccgg aggcgatcga gtctgtcttc   2880
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136 cgttcaagcg acccaagtac tgaagtacta atttaaatga tcttttagcc tgtatctata   3240
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144 <211> LENGTH: 2448
145 <212> TYPE: DNA
146 <213> ORGANISM: Aspergillus nidulans
148 <220> FEATURE:
149 <221> NAME/KEY: variation
150 <222> LOCATION: (1632)..(1632)
151 <223> OTHER INFORMATION: R = A, C, G, or T
154 <400> SEQUENCE: 2
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159 cccgtcgatc accataatcc ccctttcccc gaccagaacc tcaaagatcc atacgaaac    180
161 gacaatagtg cgaccggcag tggggctcct ccgcctgcgt tggtagagcc agaagaatac   240
163 caacgaccac cactttacac agattcagat gacagcccaa ctccgtcaaa agaacgcctg   300
165 gacaccccga gcaatgtccc atctcaggag cctgaatttg atgccgccag acttcagacg   360
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169 aagccgatgc ccgaacggca tccagtcagt ccggaggctt tgatcaagct gccaaccggg   480
171 caatcaaagg aactccccca actgcaagct aagttcaagg acgagtcgtc ctcggacaag   540
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(handwritten annotation): Per Sequence Rules, "r" can only represent "a or g." Use "n" to represent a, c, g, or t.

(the "R = A, C, G, or T" in line 151 is circled; "(1632)" in line 150 is struck through)

RAW SEQUENCE LISTING   DATE: 09/17/2004
PATENT APPLICATION: **US/10/089,211A**   TIME: 10:04:37

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

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        241 <213> ORGANISM: Aspergillus nidulans
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        250                 20                  25                  30
        253 Leu Gln Ser Trp Val Pro Pro Pro Val Asp His His Asn Pro Pro
        254             35                  40                  45
        257 Phe Pro Asp Gln Asn Leu Lys Asp Pro Thr Glu Asn Asp Asn Ser Ala
        258         50                  55                  60
        261 Thr Gly Ser Gly Ala Pro Pro Pro Ala Leu Val Glu Pro Glu Glu Thr
        262 65                  70                  75                  80
        265 Gln Arg Pro Pro Leu Thr Thr Asp Ser Asp Asp Ser Pro Thr Pro Ser
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277 Glu Asp Asp Glu Asp Ile Val Pro Ile Ser His Trp Lys Pro Met Pro
278         130             135             140
281 Glu Arg His Pro Val Ser Pro Glu Ala Leu Ile Lys Leu Pro Thr Gly
282 145             150             155                 160
285 Gln Ser Lys Glu Leu Pro Gln Leu Gln Ala Lys Phe Lys Asp Glu Ser
286             165             170             175
289 Ser Ser Asp Lys Met Gln Arg Leu Gln Gln Leu Asp Thr Ile Lys Ser
290             180             185             190
293 Ala Phe Leu His Ala Trp Asn Gly Thr Lys Ile Ser Ala Met Gly His
294         195             200             205
297 Asp Glu Val Arg Pro Leu Arg Gly Gly Phe Lys Asp Thr Phe Asn Gly
298         210             215             220
301 Trp Gly Ala Thr Leu Val Asp Ala Leu Asp Thr Leu Trp Ile Met Asp
302 225             230             235             240
305 Leu Lys Glu Glu Phe Ser Met Ala Val Asp Thr Val Lys Lys Ile Asp
306             245             250             255
309 Phe Thr Thr Ser Thr Lys Lys Glu Ile Pro Val Phe Glu Thr Thr Ile
310             260             265             270
313 Arg Thr Leu Gly Gly Met Leu Gly Ala Thr Asp Ile Ser Gly His Lys
314         275             280             285
317 Thr Asp Ile Leu Leu Glu Lys Ser Val Glu Leu Ala Asp Val Leu Met
318         290             295             300
321 Asp Ala Phe Asp Thr Pro Asn Arg Met Pro Thr Leu Thr Thr Lys Trp
322 305             310             315             320
325 Ser Pro Glu Thr Ala Ser Glu Phe Arg Arg Gly Asp Phe Lys Ala Val
326             325             330             335
329 Leu Ala Glu Leu Gly Ser Leu Ser Leu Glu Phe Thr Arg Leu Ala Gln
330             340             345             350
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334         355             360             365
337 Glu Leu Glu Lys Thr Gln Asp Leu Thr Lys Leu Pro Gly Leu Trp Pro
338         370             375             380
341 Leu Asn Leu Asp Ala Ser Gly Cys Arg Arg Val Pro Gly Val Ser Arg
342 385             390             395             400
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346             405             410             415
349 Asn Ser Thr Ser Ser Val Ser Thr Arg Thr Arg Gln Ile His Glu Gly
350             420             425             430
353 Gly Glu Pro Val Arg His Asp Asn Asp Ser Phe Glu Thr Gly Phe Pro
354         435             440             445
357 Val Ser Val Asp Thr Arg Thr Pro Pro Pro Lys Gln Asp Cys Thr Gly
358         450             455             460
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362 465             470             475             480
365 Leu Gly Asp Ser Thr Thr Glu Thr Leu Pro Lys Glu Thr Met Leu Leu
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366                   485                490               495
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370                   500                505               510
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374         515              520                525
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378     530              535                540
381 Asn Pro Pro Gly Arg Thr Thr Phe Ala Thr Glu Gly Thr His Leu Thr
382 545              550                555               560
385 Cys Phe Ala Gly Gly Met Leu Ala Ile Gly Ala Lys Leu Phe Gly Leu
386                   565                570               575
389 Asp Lys Asp Leu Lys Leu Gly Ser Gln Leu Thr Asp Gly Cys Val Trp
390         580              585                590
393 Ala Thr Glu Ala Thr Lys Ser Gly Ile Met Pro Glu Ala Phe Gln Leu
394         595              600                605
397 Val Pro Cys Lys Lys Gly Glu Pro Cys Glu Trp Asp Glu Asp Ala Thr
398     610              615                620
401 Thr Met Ala Met Asp Pro Thr Ala Asp Lys Arg Pro Ile Ser His Asn
402 625              630                635               640
405 Lys Arg Ser Ala Gly Pro Glu Lys Gly Asn Trp His Val Val Ala Thr
406                   645                650               655
409 Ala Glu Ser Ser Ser Pro Gln Glu Asp Lys Thr Gln Lys Ser Thr Thr
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414         675              680                685
417 His Glu Glu Phe Val Thr Gly Lys Ile Leu Asn Asp Arg Leu Pro Pro
418     690              695                700
421 Gly Met Thr Gly Ile Ser Ala Arg Gln Thr Leu Leu Arg Pro Glu Ala
422 705              710                715               720
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426                   725                730               735
429 Arg Glu Lys Gly Trp Lys Met Phe Gln Ala Val Asp Lys Ala Thr Lys
430         740              745                750
433 Thr Glu Leu Ala Asn Ser Ala Ile Ser Asp Val Thr Val Asp Asn Pro
434         755              760                765
437 Arg Pro Val Asp Ser Met Glu Ser Phe Trp Leu Ala Glu Thr Leu Lys
438     770              775                780
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      g, t, or u; and h represents a, c, t, or u
<222> LOCATION: (1)..(29)
<223> OTHER INFORMATION:
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      ggyggyctng gygartcntt ctacgagta                                    29
```

invalid <213> response. See item 10 on Error Summary Sheet.

Explanations go on <223> line, not <221> line. See 1.823 Sequence Rules.

same errors in Sequence 16

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/17/2004
PATENT APPLICATION: **US/10/089,211A**   TIME: 10:04:38

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1632
Seq#:8; N Pos. 4
Seq#:15; N Pos. 9,18
Seq#:16; N Pos. 4,13,16,22,25

IMPORTANT (see item 2 on Error Summary sheet)

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:15; Line(s) 812
Seq#:16; Line(s) 827

L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1620
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:817 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:814
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:832 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:829
L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0